38. Peptide nucleic acid probe according to claim 37, said probe hybridising to a target sequence of mycobacterial rDNA, precursor rRNA, or 23S, 16S or 5S rRNA forming detectable hybrids, or a mixture of such probes.

39. Peptide nucleic acid probe according to claim 37, said probe hybridising to a target sequence of mycobacterial rDNA, precursor rRNA, or 23S, 16S or 5S rRNA forming detectable hybrids, said target sequence being obtainable by

a) comparing the nucleobase sequences of said mycobacterial rRNA or rDNA of one or more mycobacteria to be detected with the corresponding nucleobase sequence of organism(s), from which said one or more mycobacteria are to be distinguished,

b) selecting a target sequence of said rRNA or rDNA which includes at least one nucleobase differing from the corresponding nucleobase of the organism(s), from which said one or more mycobacteria are to be distinguished, and

c) determining the capability of said probe to hybridise to the selected target sequence to form detectable hybrids,

or a mixture of such probes.

40. Peptide nucleic acid probe according to claim 37, said probe hybridising to a target sequence of mycobacterial rDNA, precursor rRNA or 23S, 16S or 5S rRNA forming detectable hybrids, said probe being obtainable by

a) comparing the nucleobase sequences of said mycobacterial rRNA or rDNA of one or more mycobacteria to be detected with the corresponding nucleobase sequence of organism(s), from which said one or more mycobacteria are to be distinguished,

b) selecting a target sequence of said rRNA or rDNA which includes at least one nucleobase differing from the corresponding nucleobase of the organism(s), from which said one or more mycobacteria are to be distinguished,

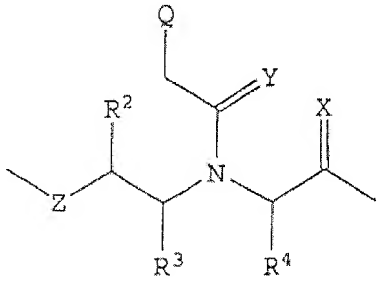
c) synthesising said probe, and

d) determining the capability of said probe to hybridise to the selected target sequence to form detectable hybrids,

or a mixture of such probes.

41. Peptide nucleic acid probe according to claim 37, for detecting a target sequence of one or more mycobacteria of the Mycobacterium tuberculosis Complex (MTC) or for detecting a target sequence of one or more mycobacteria other than mycobacteria of the Mycobacterium tuberculosis Complex (MOTT) present in a sample, which probe comprises from 6 to 30 polymerised peptide nucleic acid moieties, said probe hybridising to a target sequence of mycobacterial rDNA, precursor rRNA or 23S, 16S or 5S rRNA forming detectable hybrids, or a mixture of such probes.

42. Peptide nucleic acid probe according to claim 37, for detecting a target sequence of rDNA, precursor rRNA or 23S, 16S or 5S rRNA of one or more mycobacteria of the Mycobacterium tuberculosis Complex (MTC) or for detecting a target sequence of rDNA, precursor rRNA or 23S, 16S or 5S rRNA of one or more mycobacteria other than mycobacteria of the Mycobacterium tuberculosis Complex (MOTT) present in a sample, which probe comprises from 10 to 30 polymerised moieties of formula (I)



(I)

wherein each X and Y independently designate O or S,

each Z independently designates O, S, NR^1, or $C(R^1)_2$, wherein each R^1 independently designate H, C_{1-6} alkyl, C_{1-6} alkenyl, C_{1-6} alkynyl,

each R^2, R^3 and R^4 designate independently H, the side chain of a naturally occurring amino acid, the side chain of a non-naturally occurring amino acid, C_{1-4} alkyl, C_{1-4} alkenyl or C_{1-4} alkynyl, or a functional group, each Q independently designates a naturally occurring nucleobase, a non-naturally occurring nucleobase, an intercalator, a nucleobase-binding group, a label or H,

C2

with the proviso that the probe comprising such subsequence forms detectable hybrids with the target sequence of said mycobacterial rDNA, precursor rRNA or 23S, 16S or 5S rRNA, or a mixture of such probes.

43. Peptide nucleic acid probe according to claim 42, for detecting a target sequence of 23S rRNA of one or more mycobacteria of the Mycobacterium tuberculosis Complex (MTC) present in a sample, which probe comprises from 10 to 30 polymerised moieties of formula (I),

with the proviso that the Qs of adjacent moieties are selected so as to form a sequence of which a subsequence includes at least one nucleobase that is complementary to a nucleobase of M. tuberculosis 23S rRNA differing from the corresponding nucleobase of at least M. avium located within the following domains

positions 149-158 in Figure 1A,

positions 220-221 in Figure 1A,

positions 328-361 in Figure 1A and Figure 1B,

positions 453-455 in Figure 1B,

positions 490-501 in Figure 1B,

positions 637-660 in Figure 1C,

positions 706-712 in Figure 1D,

positions 762-789 in Figure 1D,
position 989 in Figure 1D,
positions 1068-1072 in Figure 1D,
position 1148 in Figure 1E,
positions 1311-1329 in Figure 1E,
positions 1361-1364 in Figure 1F,
position 1418 in Figure 1F,
positions 1563-1570 in Figure 1F,
positions 1627-1638 in Figure 1G,
positions 1675-1677 in Figure 1G,
position 1718 in Figure 1G,
positions 1734-1740 in Figure 1H,
positions 1967-1976 in Figure 1H,
positions 2403-2420 in Figure 1H,
positions 2457-2488 in Figure 1I,
positions 2952-2956 in Figure 1I,
positions 2966-2969 in Figure 1J,
positions 3000-3003 in Figure 1J or
positions 3097-3106 in Figure 1J,

and further with the proviso that the probe comprising such subsequence forms detectable hybrids with a target sequence of said mycobacterial 23S rRNA, or a mixture of such probes.

44. Peptide nucleic acid probe according to claim 42, for detecting a target sequence of 16S rRNA of one or more mycobacteria of the Mycobacterium tuberculosis Complex (MTC) present in a sample, which probe comprises from 10 to 30 polymerised moieties of formula (I),

with the proviso that the Qs of adjacent moieties are selected so as to form a sequence of which a subsequence includes at least one nucleobase that is complementary to a nucleobase of M. tuberculosis 16S rRNA differing from the corresponding nucleobase of at least M. avium located within the following domains

positions 76-79 in Figure 2A,
positions 98-101 in Figure 2A,
positions 135-136 in Figure 2 A,
positions 194-201 in Figure 2B,
positions 222-229 in Figure 2B,
position 242 in Figure 2B,
position 474 in Figure 2C,
positions 1136-1145 in Figure 2C,
positions 1271-1272 in Figure 2C,
positions 1287-1292 in Figure 2D,
position 1313 in Figure 2D, or
position 1334 in Figure 2D,

and further with the proviso that the probe comprising such subsequence forms detectable hybrids with a target sequence of said mycobacterial 16S rRNA, or a mixture of such probes.

45. Peptide nucleic acid probe according to claim 42, for detecting a target sequence of 5S rRNA of one or more mycobacteria of the Mycobacterium tuberculosis Complex (MTC) [optionally] present in a sample, which probe comprises from 10 to 30 polymerised moieties of formula (I),

with the proviso that the Qs of adjacent moieties are selected so as to form a sequence of which a subsequence includes at least one nucleobase that is complementary to a nucleobase of M. tuberculosis 5S rRNA differing from the corresponding nucleobase of at least M. avium located within the following domain

positions 86-90 in Figure 3

and further with the proviso that the probe comprising such subsequence forms detectable hybrids with a target sequence of said mycobacterial 5S rRNA, or a mixture of such probes.

46. Peptide nucleic acid probe according to claim 42, for detecting a target sequence of 23S or 16S rRNA of one or more mycobacteria of the Mycobacterium tuberculosis Complex (MTC) present in a sample, which probe comprises from 10 to 30 polymerised moieties of formula (I),

Cr

with the proviso that the Qs of adjacent moieties are selected so as to form a sequence of which a subsequence includes at least one nucleobase that is complementary to a nucleobase of M. tuberculosis 23S or 16 S rRNA differing from the corresponding nucleobase of at least M. avium located within the following domains

positions 149-158 in Figure 1A,
positions 328-361 in Figure 1A and Figure 1B,
positions 490-501 in Figure 1B,
positions 637-660 in Figure 1C,
positions 762-789 in Figure 1D,
positions 1068-1072 in Figure 1D,
positions 1311-1329 in Figure 1E,
positions 1361-1364 in Figure 1F,
positions 1563-1570 in Figure 1F,
positions 1627-1638 in Figure 1G,
positions 1734-1740 in Figure 1H,
positions 2457-2488 in Figure 1I,
positions 2952-2956 in Figure 1I,
positions 3097-3106 in Figure 1J,
positions 135-136 in Figure 2 A, or

positions 1287-1292 in Figure 2D,

and further with the proviso that the probe comprising such subsequence forms detectable hybrids with a target sequence of said mycobacterial 23S or 16S rRNA, or a mixture of such probes.

47. Peptide nucleic acid probe according to claim 42, for detecting a target sequence of 23S rRNA of one or more mycobacteria other than mycobacteria of the Mycobacterium tuberculosis Complex (MOTT) present in a sample, which probe comprises from 10 to 30 polymerised moieties of formula (I),

with the proviso that the Qs of adjacent moieties are selected so as to form a sequence of which a subsequence includes at least one nucleobase that is complementary to a nucleobase of M. avium 23S rRNA differing from the corresponding nucleobase of at least M. tuberculosis located within the following domains

positions 99-101 in Figure 4A,
position 183 in Figure 4A,
positions 261-271 in Figure 4A,
positions 281-284 in Figure 4B,
positions 290-293 in Figure 4B,
positions 327-335 in Figure 4B,
positions 343-357 in Figure 4B,
positions 400-405 in Figure 4B and Figure 4C,
positions 453-462 in Figure 4C,
positions 587-599 in Figure 4C,
positions 637-660 in Figure 4D,
positions 704-712 in Figure 4D,
positions 763-789 in Figure 4E,
positions 1060-1074 in Figure 4E,

positions 1177-1185 in Figure 4E,
positions 1259-1265 in Figure 4F,
positions 1311-1327 in Figure 4F,
positions 1345-1348 in Figure 4F,
positions 1361-1364 in Figure 4G,
positions 1556-1570 in Figure 4G,
positions 1608-1613 in Figure 4H,
positions 1626-1638 in Figure 4H,
C2 positions 1651-1659 in Figure 4H,
positions 1675-1677 in Figure 4H,
positions 1734-1741 in Figure 4H,
positions 1847-1853 in Figure 4I,
positions 1967-1976 in Figure 4I,
positions 2006-2010 in Figure 4I,
positions 2025-2027 in Figure 4I,
positions 2131-2132 in Figure 4J,
positions 2252-2255 in Figure 4J,
positions 2396-2405 in Figure 4J and Figure 4K,
positions 2416-2420 in Figure 4K,
positions 2474-2478 in Figure 4K,
position 2687 in Figure 4K,
position 2719 in Figure 4K,
position 2809 in Figure 4L,
positions 3062-2068 in Figure 4L, or
positions 3097-3106 in Figure 4L,

and further with the proviso that the probe comprising such subsequence forms detectable hybrids with a target sequence of said mycobacterial 23S rRNA, or a mixture of such probes.

48. Peptide nucleic acid probe according to claim 42, for detecting a target sequence of 16S rRNA of one or more mycobacteria other than mycobacteria of the Mycobacterium tuberculosis Complex (MOTT) present in a sample, which probe comprises from 10 to 30 polymerised moieties of formula (I),

with the proviso that the Qs of adjacent moieties are selected so as to form a sequence of which a subsequence includes at least one nucleobase that is complementary to a nucleobase of M. avium 16S rRNA differing from the corresponding nucleobase of at least M. tuberculosis located within the following domains

C7

positions 135-136 in Figure 5A,
positions 472-475 in Figure 5A,
positions 1136-1144 in Figure 5A,
positions 1287-1292 in Figure 5B,
position 1313 in Figure 5B, or
position 1334 in Figure 5B,

and further with the proviso that the probe comprising such subsequence forms detectable hybrids with a target sequence of said mycobacterial 16S rRNA, or a mixture of such probes.

49. Peptide nucleic acid probe according to claim 42, for detecting a target sequence of 23S or 16S rRNA of one or more mycobacteria other than mycobacteria of the Mycobacterium tuberculosis Complex (MOTT) present in a sample, which probe comprises from 10 to 30 polymerised moieties of formula (I),

with the proviso that the Qs of adjacent moieties are selected so as to form a sequence of which a subsequence includes at least one nucleobase that is complementary to a nucleobase of M. avium 23S or 16S rRNA differing from the corresponding nucleobase of at least M. tuberculosis located within the following domains

positions 99-101 in Figure 4A,
positions 290-293 in Figure 4B,

positions 400-405 in Figure 4B and Figure 4C,
positions 453-462 in Figure 4C,
positions 637-660 in Figure 4D,
positions 763-789 in Figure 4E,
positions 1311-1327 in Figure 4F,
positions 1361-1364 in Figure 4G,
positions 1734-1741 in Figure 4H,
C2 positions 2025-2027 in Figure 4I,
positions 2474-2478 in Figure 4K,
positions 3062-2068 in Figure 4L, or
positions 1287-1292 in Figure 5B,

and further with the proviso that the probe comprising such subsequence forms detectable hybrids with a target sequence of said mycobacterial 23S or 16S rRNA, or a mixture of such probes.

50. Peptide nucleic acid probe according to claim 42, for detecting a target sequence of 23S, 16S or 5S rRNA of one or more mycobacteria of the Mycobacterium tuberculosis Complex (MTC) or for detecting a target sequence of 23S, 16S or 5S rRNA of one or more mycobacteria other than mycobacteria of the Mycobacterium tuberculosis Complex (MOTT) present in a sample, which probe comprises from 10 to 30 polymerised moieties of formula (I),

with the proviso that the Qs of adjacent moieties are selected so as to form a sequence of which a subsequence includes at least one nucleobase that is complementary to a nucleobase that differs from the corresponding nucleobase of 23S, 16S or 5S rRNA of said one or more mycobacteria located within the following domains

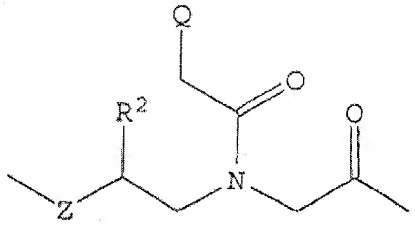
positions 2568-2569 in Figure 6,
position 452 in Figure 7,

positions 473-477 in Figure 7, or

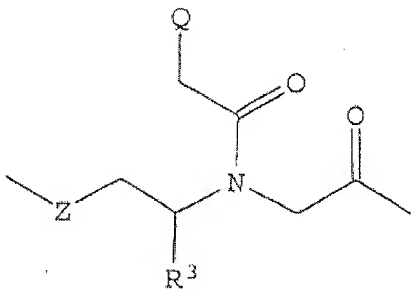
positions 865-866 in Figure 7,

and further with the proviso that the probe comprising such subsequence forms detectable hybrids with the target sequence of said mycobacterial 23S, 16S or 5S rRNA, or a mixture of such probes.

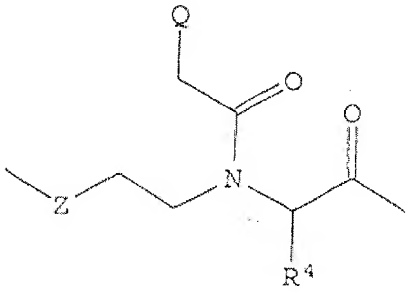
51. Peptide nucleic acid probe according to claim 42, of formula (II), (III), or (IV)



(II)



(III)



(IV)

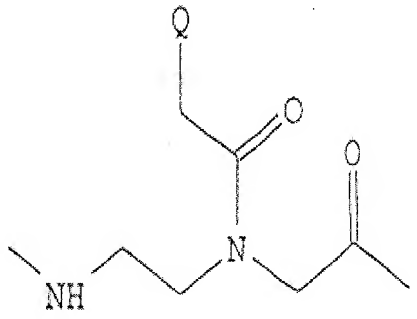
wherein Z, R^2, R^3, and R^4, and Q are as defined for the formula (I),
or a mixture of such probes.

52. Peptide nucleic acid probe according to claim 42, wherein Z is NH, NCH_3 or O, each R^2, R^3 and R^4 independently designate H or the side chain of a naturally occurring amino acid, the side chain of a non-naturally occurring amino acid, or C_{1-4} alkyl, and each Q is a naturally occurring nucleobase or a non-naturally occurring nucleobase, or a mixture of such probes.

CV

53. Peptide nucleic acid probe according to claim 42, wherein Z is NH or O, and R^2 is H or the side chain of Ala, Asp, Cys, Glu, His, HomoCys, Lys, Orn, Ser or Thr, and Q is a nucleobase selected from thymine, adenine, cytosine, guanine, uracil, iso-C and 2,6-diaminopurine, or a mixture of such probes.

54. Peptide nucleic acid probe according to claim 53, of formula (V)



(V)

wherein R^4 is H or the side chain of Ala, Asp, Cys, Glu, His, HomoCys, Lys, Orn, Ser or Thr, and Q is as defined in claim 53, or a mixture of such probes.

55. Peptide nucleic acid probe according to claim 42, further comprising one or more labels, or a mixture of such probes, which labels may be mutually identical or different, which probes may comprise one or more linkers, and which probes may be mutually identical or different.

56. Peptide nucleic acid probe according to claim 37, for detecting a target sequence of one or more mycobacteria, the nucleobase sequence of said probe being substantially complementary to the nucleobase sequence of said target sequence.

57. Peptide nucleic acid probe according to claim 37, for detecting a target sequence of one or more mycobacteria, the nucleobase sequence of said probe being complementary to the nucleobase sequence of said target sequence.

58. Peptide nucleic acid probe according to claim 42, wherein the Qs of adjacent moieties are selected so as to form one of the following subsequences

AGA TGC GGG TAG CAC (SEQ ID NO: 1)
TGT TTT CTC CTC CTA (SEQ ID NO: 2)
ACT GCC TCT CAG CCG (SEQ ID NO: 3)
TGA TAC TAG GCA GGT (SEQ ID NO: 4)
CGG ATT CAC AGC GGA (SEQ ID NO: 5)
TCA CCA CCC TCC TCC (SEQ ID NO: 6)
TTA ACC TTG CGA CAT (SEQ ID NO: 7)
ACT ATT CAC ACG CGC (SEQ ID NO: 8)
CTC CGC GGT GAA CCA (SEQ ID NO: 9)
GCT TTA CAC CAC GGC (SEQ ID NO: 10)
ACG CTT GGG GGC CTT (SEQ ID NO: 11)
CCA CAC CCA CCA CAA (SEQ ID NO: 12)

CCG GTG GCT TCG CTG (SEQ ID NO: 13)
ACT TGC CTT GTC GCT (SEQ ID NO: 14)
GAT TCG TCA CGG GCG (SEQ ID NO: 15)
AAC TCC ACA CCC CCG (SEQ ID NO: 16)
ACT CCA CAC CCC CGA (SEQ ID NO: 17)
ACC CCT TCG CTT GAC (SEQ ID NO: 18)
CTT GCC CCA GTG TTA (SEQ ID NO: 19)
CTC TCC CTA CCG GCT (SEQ ID NO: 20)
GAT ATT CCG GTC CCC (SEQ ID NO: 21)
ACT CCG CCC CAA CTG (SEQ ID NO: 22)
CTG TCC CTA AAC CCG (SEQ ID NO: 23)
TTC GAG GTT AGA TGC (SEQ ID NO: 24)
GTC CCT AAA CCC GAT (SEQ ID NO: 25)
GGT GCA CCA GAG GTT (SEQ ID NO: 26)
CTG GCG GGA CAA CTG (SEQ ID NO: 27)
TTA TCC TGA CCG AAC (SEQ ID NO: 28)
GAC CTA TTG AAC CCG (SEQ ID NO: 29)
GAA GAG ACC TTT CCG (SEQ ID NO: 30)
CAC TCG AGT ATC TCC (SEQ ID NO: 31)
ATC ACC CAC GTG TTA (SEQ ID NO: 32)
GCA TCC CGT GGT CCT (SEQ ID NO: 33)
CAC AAG ACA TGC ATC (SEQ ID NO: 34)
TAA AGC GCT TTC CAC (SEQ ID NO: 35)
GCT CAT CCC ACA CCG (SEQ ID NO: 36)
CCG AGA GAA CCC GGA (SEQ ID NO: 37)
AGT CCC CAC CAT TAC (SEQ ID NO: 38)
AAC CTC GCG GCA TCG (SEQ ID NO: 39)

GGC TTT TAA GGA TTC (SEQ ID NO: 40)
GAC CCC GAT CCG AAC (SEQ ID NO: 41)
CCG ACT TCA CGG GGT (SEQ ID NO: 42)
CGG AGG GGC AGT ATC (SEQ ID NO: 43)
GAT CAA TGC TCG GTT (SEQ ID NO: 44)
TTC CCC GCG TTA CCT (SEQ ID NO: 45)
TTA GCC TGT TCC GGT (SEQ ID NO: 46)
GCA TGC GGT TTA GCC (SEQ ID NO: 47)
TAC CCG GTT GTC CAT (SEQ ID NO: 48)
GTA GAG CTG AGA CAT (SEQ ID NO: 49)
GCC GTC CCA GGC CAC (SEQ ID NO: 50)
CTC GGG TGT TGA TAT (SEQ ID NO: 51)
ACT ATT TCA CTC CCT (SEQ ID NO: 52)
ACG CCA TCA CCC CAC (SEQ ID NO: 53)
CGA CGT GTC CCT GAC (SEQ ID NO: 54)
ACT ACA CCC CAA AGG (SEQ ID NO: 55)
CAC GCT TTT ACA CCA (SEQ ID NO: 56)
GCG ACT ACA CAT CCT (SEQ ID NO: 57)
CGG CGC ATA ATC ACT (SEQ ID NO: 58)
CCA CAT CCA CCG TAA (SEQ ID NO: 59)
CGC TGA ATG GGG GAC (SEQ ID NO: 60)
GGA GCT TCG CTG AAT (SEQ ID NO: 61)
CGG TCA CCC GGA GCT (SEQ ID NO: 62)
GGA CGC CCA TAC ACG (SEQ ID NO: 63)
GAA GGG GAA TGG TCG (SEQ ID NO: 64)
AAT CGC CAC GCC CCC (SEQ ID NO: 65)
CAG CGA AGG TCC CAC (SEQ ID NO: 66)

GTC ACC CCA TTG CTT (SEQ ID NO: 67)
ATC GCT CTC TAC GGG (SEQ ID NO: 68)
GTG TAT GTG CTC GCT (SEQ ID NO: 69)
ACG GTA TTC CGG GCC (SEQ ID NO: 70)
GGC CGA ATC CCG CTC (SEQ ID NO: 71)
AAA CAG TCG CTA CCC (SEQ ID NO: 72)
C2 CCT TAC GGG TTA ACG (SEQ ID NO: 73)
GAG ACA GTT GGG AAG (SEQ ID NO: 74)
TGG CGT CTG TGC TTC (SEQ ID NO: 75)
CGA CTC CAC ACA AAC (SEQ ID NO: 76)
GAT AAG GGT TCG ACG (SEQ ID NO: 77)
ATC CGT TGA GTG ACA (SEQ ID NO: 78)
CAG CCC GTT ATC CCC (SEQ ID NO: 79)
AAC CTT TGG GAC CTG (SEQ ID NO: 80)
TAA AAG GGT GAG AAA (SEQ ID NO: 81)
GTC TGG CCT ATC AAT (SEQ ID NO: 82)
AGA TTG CCC ACG TGT (SEQ ID NO: 83)
AAT CCG AGA AAA CCC (SEQ ID NO: 84)
GCA TTA CCC GCT GGC (SEQ ID NO: 85)
TTA AAA GGA TTC GCT (SEQ ID NO: 86)
AGA CCC CAA TCC GAA (SEQ ID NO: 87)
GAC TCC GAC TTC ATG (SEQ ID NO: 88)
GTC TTT TCG TCC TGC (SEQ ID NO: 89)
GTC TTA TCG TCC TGC (SEQ ID NO: 90)
GTC TTC TCG TCC TGC (SEQ ID NO: 91)
GTC TTG TCG TCC TGC (SEQ ID NO: 92)
GTC TAT TCG TCC TGC (SEQ ID NO: 93)

GTC TCT TCG TCC TGC (SEQ ID NO: 94)

GTC TGT TCG TCC TGC (SEQ ID NO: 95)

TTG GCC GGT GCT TCT (SEQ ID NO: 96)

TTG GCC GGT ACT TCT (SEQ ID NO: 97)

TTG GCC GGT CCT TCT (SEQ ID NO: 98)

TTG GCC GGT TCT TCT (SEQ ID NO: 99)

ACC GCG GCT GCT GGC (SEQ ID NO: 100)

ACC GCG GCT ACT GGC (SEQ ID NO: 101)

ACC GCG GCT CCT GGC (SEQ ID NO: 102)

ACC GCG GCT TCT GGC (SEQ ID NO: 103)

CGG CAG CTG GCA CGT (SEQ ID NO: 104)

CGG CCG CTG GCA CGT (SEQ ID NO: 105)

CGG CTG CTG GCA CGT (SEQ ID NO: 106)

CGT ATT ACC GCA GCT (SEQ ID NO: 107)

CGT ATT ACC GCC GCT (SEQ ID NO: 107)

CGT ATT ACC GCT GCT (SEQ ID NO: 109)

TTC CTT TGA GTT TTA (SEQ ID NO: 110)

TTC CTT TAA GTT TTA (SEQ ID NO: 111)

TTC CTT TCA GTT TTA (SEQ ID NO: 112)

TTC CTT TTA GTT TTA (SEQ ID NO: 113)

TTC CTT AGA GTT TTA (SEQ ID NO: 114)

TTC CTT CGA GTT TTA (SEQ ID NO: 115)

TTC CTT GGA GTT TTA (SEQ ID NO: 116)

CAT GTG TCC TGT GGT (SEQ ID NO: 117)

CGT CAG CCC GAG AAA (SEQ ID NO: 118)

CAC TAC ACA CGC TCG (SEQ ID NO: 119)

TGG CGT TGA GGT TTC (SEQ ID NO: 120)

AAC ACT CCC TTT GGA (SEQ ID NO: 123)

or a mixture of such probes.

59. Peptide nucleic acid probe according to claim 58, wherein the Qs of adjacent moieties are selected so as to form one the following subsequences

TCA CCA CCC TCC TCC (SEQ ID NO: 6)
CCA CCC TCC TCC (modified SEQ ID NO: 6)
ACT ATT CAC ACG CGC (SEQ ID NO: 8)
CCA CAC CCA CCA CAA (SEQ ID NO: 12)
AAC TCC ACA CCC CCG (SEQ ID NO: 16)
ACT CCA CAC CCC CGA (SEQ ID NO: 17)
ACT CCG CCC CAA CTG (SEQ ID NO: 22)
CTG TCC CTA AAC CCG (SEQ ID NO: 23)
TTC GAG GTT AGA TGC (SEQ ID NO: 24)
GTC CCT AAA CCC GAT (SEQ ID NO: 25)
GAC CTA TTG AAC CCG (SEQ ID NO: 29)
GCA TCC CGT GGT CCT (SEQ ID NO: 33)
CAC AAG ACA TGC ATC (SEQ ID NO: 34)
GGC TTT TAA GGA TTC (SEQ ID NO: 40)
GAT CAA TGC TCG GTT (SEQ ID NO: 44)
CGA CTC CAC ACA AAC (SEQ ID NO: 76)
GCA TTA CCC GCT GGC (SEQ ID NO: 85)
GTC TTA TCG TCC TGC (SEQ ID NO: 90)
GTC TTC TCG TCC TGC (SEQ ID NO: 91)
GTC TTG TCG TCC TGC (SEQ ID NO: 92)
GTC TAT TCG TCC TGC (SEQ ID NO: 93)
GTC TCT TCG TCC TGC (SEQ ID NO: 94)

GTC TGT TCG TCC TGC (SEQ ID NO: 95)
AAC ACT CCC TTT GGA (SEQ ID NO: 123)
CAT GTG TCC TGT GGT (SEQ ID NO: 117)
CGT CAG CCC GAG AAA (SEQ ID NO: 118)
CAC TAC ACA CGC TCG, (SEQ ID NO: 119)
TGG CGT TGA GGT TTC (SEQ ID NO: 120)

C2

or a mixture of such probes.

60. Peptide nucleic acid probe according to claim 58 selected from the group consisting of

Lys(Flu)-Lys(Flu)-TCA CCA CCC TCC TCC-NH_2 (OK 446/modified SEQ ID NO: 6)

Lys(Flu)-Lys(Flu)-CCA CCC TCC TCC-NH_2 (OK 575/modified SEQ ID NO: 6)

Lys(Flu)-Lys(Flu)-ACT ATT CAC ACG CGC-NH_2 (OK 447/modified SEQ ID NO: 8)

Lys(Flu)-ACT ATT CAC ACG CGC-NH_2 (OK 688/modified SEQ ID NO: 8)

Lys(Flu)-Lys(Flu)-CCA CAC CCA CCA CAA-NH_2 (OK 448/modified SEQ ID NO: 12)

Lys(Flu)-Lys(Flu)-AAC TCC ACA CCC CCG-NH_2 (OK 449/modified SEQ ID NO: 16)

Lys(Flu)-Lys(Flu)-ACT CCA CAC CCC CGA-NH_2 (OK 309/modified SEQ ID NO: 17)

Lys(Flu)-Lys(Flu)-ACT CCG CCC CAA CTG-NH_2 (OK 450/modified SEQ ID NO: 22)

Lys(Flu)-Lys(Flu)-CTG TCC CTA AAC CCG-NH_2 (OK 305/modified SEQ ID NO: 23)

Lys(Flu)-Lys(Flu)-TTC GAG GTT AGA TGC-NH_2 (OK 306/modified SEQ ID NO: 24)

Lys(Flu)-TTC GAG GTT AGA TGC-NH_2 (OK 682/modified SEQ ID NO: 24)

Lys(Flu)-Lys(Flu)-GTC CCT AAA CCC GAT-NH_2 (OK 307/modified SEQ ID NO: 25)

Lys(Flu)-GTC CCT AAA CCC GAT-NH_2 (OK 654/modified SEQ ID NO: 25)

CV

Lys(Flu)-GAC CTA TTG AAC CCG-NH_2 (OK 660/modified SEQ ID NO: 29)

Lys(Flu)-Lys(Flu)-Gly-GCA TCC CGT GGT CCT-NH_2 (OK 223/modified SEQ ID NO: 33)

Lys(Flu)-Lys(Flu)-CAC AAG ACA TGC ATC-NH_2 (OK 310/modified SEQ ID NO: 34)

Lys(Flu)-CAC AAG ACA TGC ATC-NH_2 (OK 655/modified SEQ ID NO: 34)

Lys(Flu)-GGC TTT TAA GGA TTC-NH_2 (OK 689/modified SEQ ID NO: 40)

Lys(Rho)-GGC TTT TAA GGA TTC-NH_2 (OK 702/modified SEQ ID NO: 40)

Flu-β-Ala-β-Ala-GAT CAA TGC TCG GTT-NH_2 (OK 624/modified SEQ ID NO: 44)

Flu-β-Ala-β-Ala-CGA CTC CAC ACA AAC-NH_2 (OK 612/modified SEQ ID NO: 76)

Flu-β-Ala-β-Ala-GCA TTA CCC GCT GGC-NH_2 (OK 623/modified SEQ ID NO: 85)

Lys(Flu)-GTC TTT TCG TCC TGC-NH_2 (OK 745/modified SEQ ID NO: 89)

Lys(Rho)-GTC TTA TCG TCC TGC-NH_2 (OK 746/modified SEQ ID NO: 90)

Lys(Rho)-GTC TTC TCG TCC TGC-NH_2 (OK 746/modified SEQ ID NO: 91)

Lys(Rho)-GTC TTG TCG TCC TGC-NH_2 (OK 746/modified SEQ ID NO: 92)

Lys(Rho)-GTC TAT TCG TCC TGC-NH_2 (OK 747/modified SEQ ID NO: 93)

Lys(Rho)-GTC TCT TCG TCC TGC-NH_2 (OK 747/modified SEQ ID NO: 94)

Lys(Rho)-GTC TGT TCG TCC TGC-NH_2 (OK 747/modified SEQ ID NO: 95) and

Lys(Flu)-AAC ACT CCC TTT GGA-NH_2 (OK 749/modified SEQ ID NO: 123)
wherein Flu denotes a 5-(and 6)-carboxyfluoroescein label and Rho denotes a rhodamine label,

or a mixture of such probes.

61. Kit for detecting a target sequence of one or more mycobacteria, and/or for detecting a target sequence of one or more mycobacteria other than mycobacteria of the Mycobacterium tuberculosis Complex (MOTT), characterized in that said kit comprises at least one peptide nucleic acid probe according to claim 37, and a detection system with at least one detecting reagent.

62. Kit according to claim 61, further comprising a solid phase capture system.

REMARKS

Claims 37-62, presented hereby, are pending.

Claims 37-62 correspond to claims 1-24, 35, and 36, respectively, revised to address the rejection of record under §112, ¶2, as explained below.

The specification is amended hereby to include the §120 priority claim to the parent application.

Claims were rejected under 35 USC 112 ¶2. Reconsideration is requested in view of the changes to the claims effected by the instant amendment.

Throughout the claims, the term "being capable of hybridising" has been changed to "hybridising". Throughout the claims, the expression "is capable of forming" has been changed to "forms". Throughout the claims, the terms "optionally" and "in particular" have been deleted.

Compliance with Sequence Listing Rules, as required, is provided by filing concurrently herewith Response to Notice to Comply with Sequence Rules, including Sequence Listing on paper and computer readable form (in duplicate) and Amendment Entering Sequence Listing.